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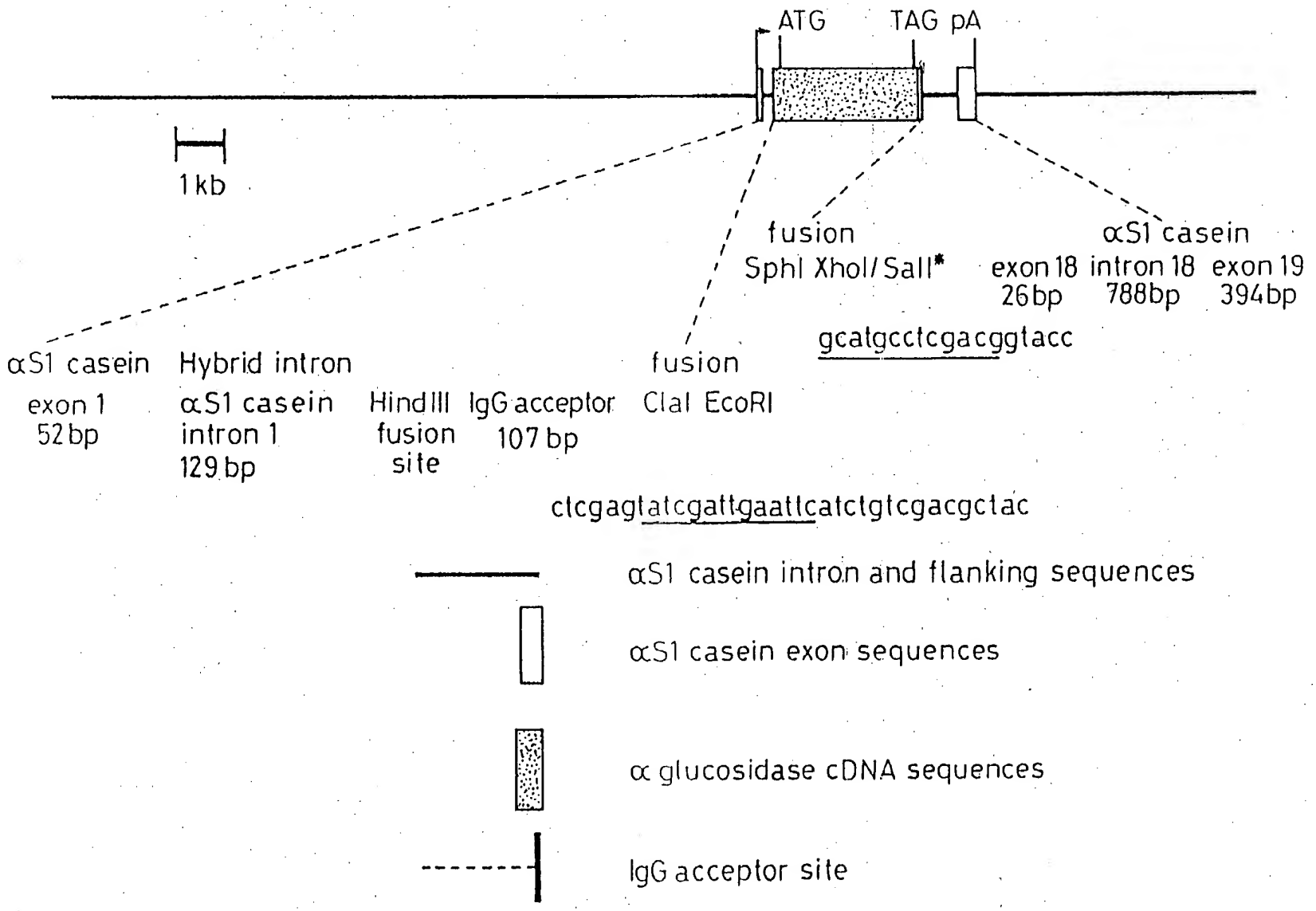
Fig. 1.



α-glucosidase constructs

Fig. 2.A

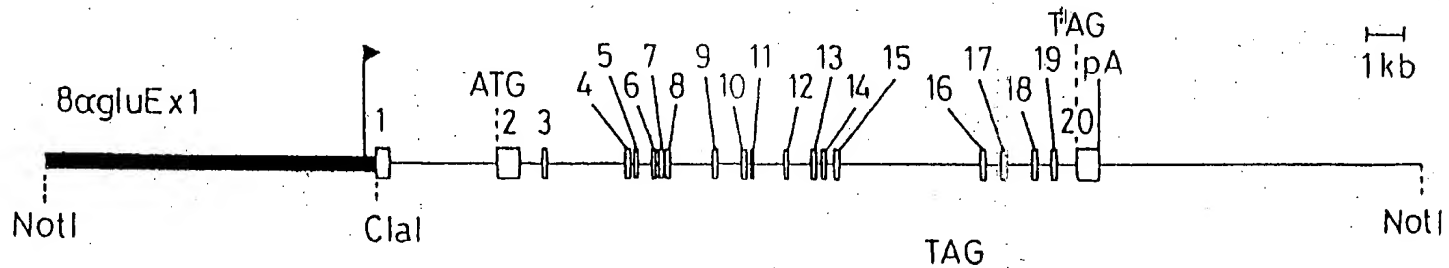


Fig. 2B.

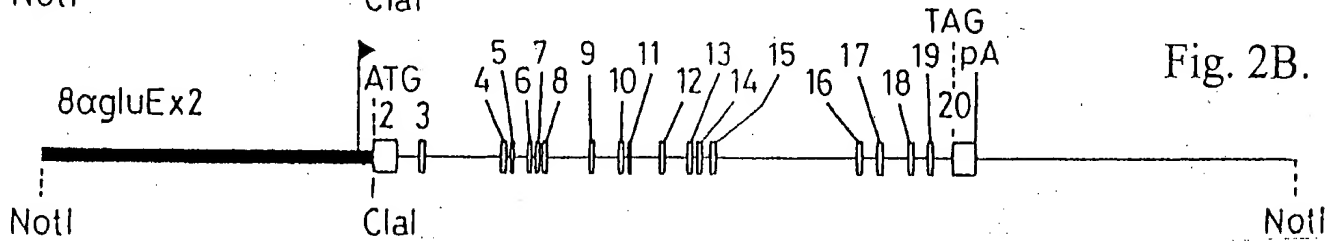
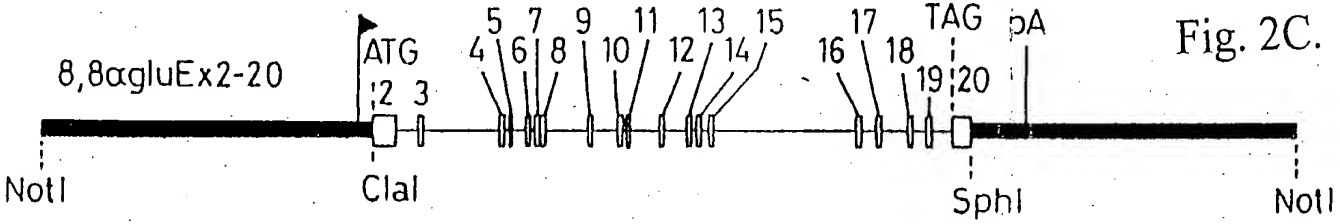


Fig. 2C.



Transcription Initiation site.

α_{S1} casein sequence, promoter or 3' untranslated region.

2 3 The boxes represent the exons in the α-glucosidase sequence, the thin line represents the intron sequences.
The numbers above the boxes are the exon numbers

pA = polyadenylation signal.
ATG = translation initiation site.
TAG = translation stop codon

Fig. 3A.

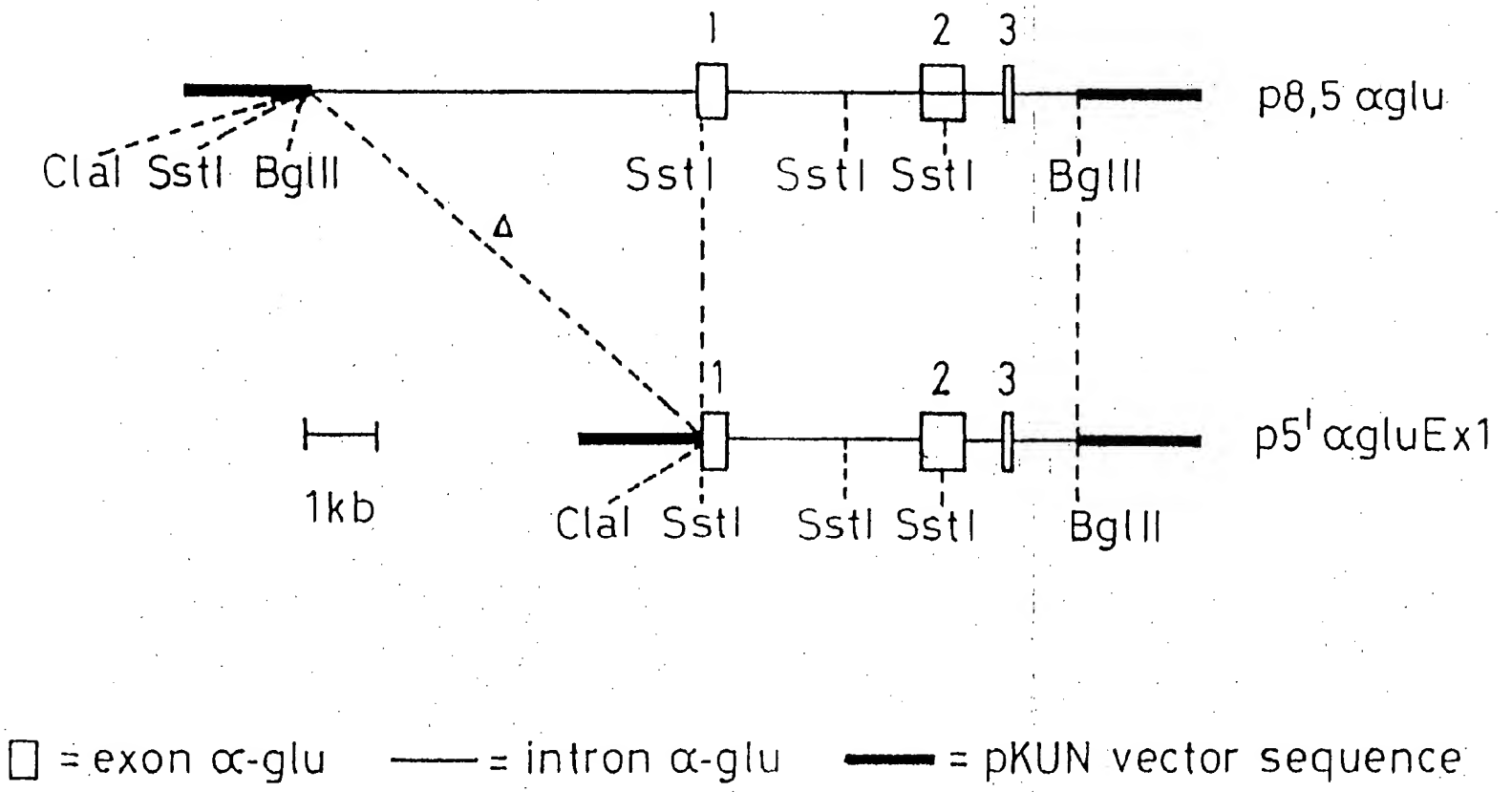


Fig. 3B.

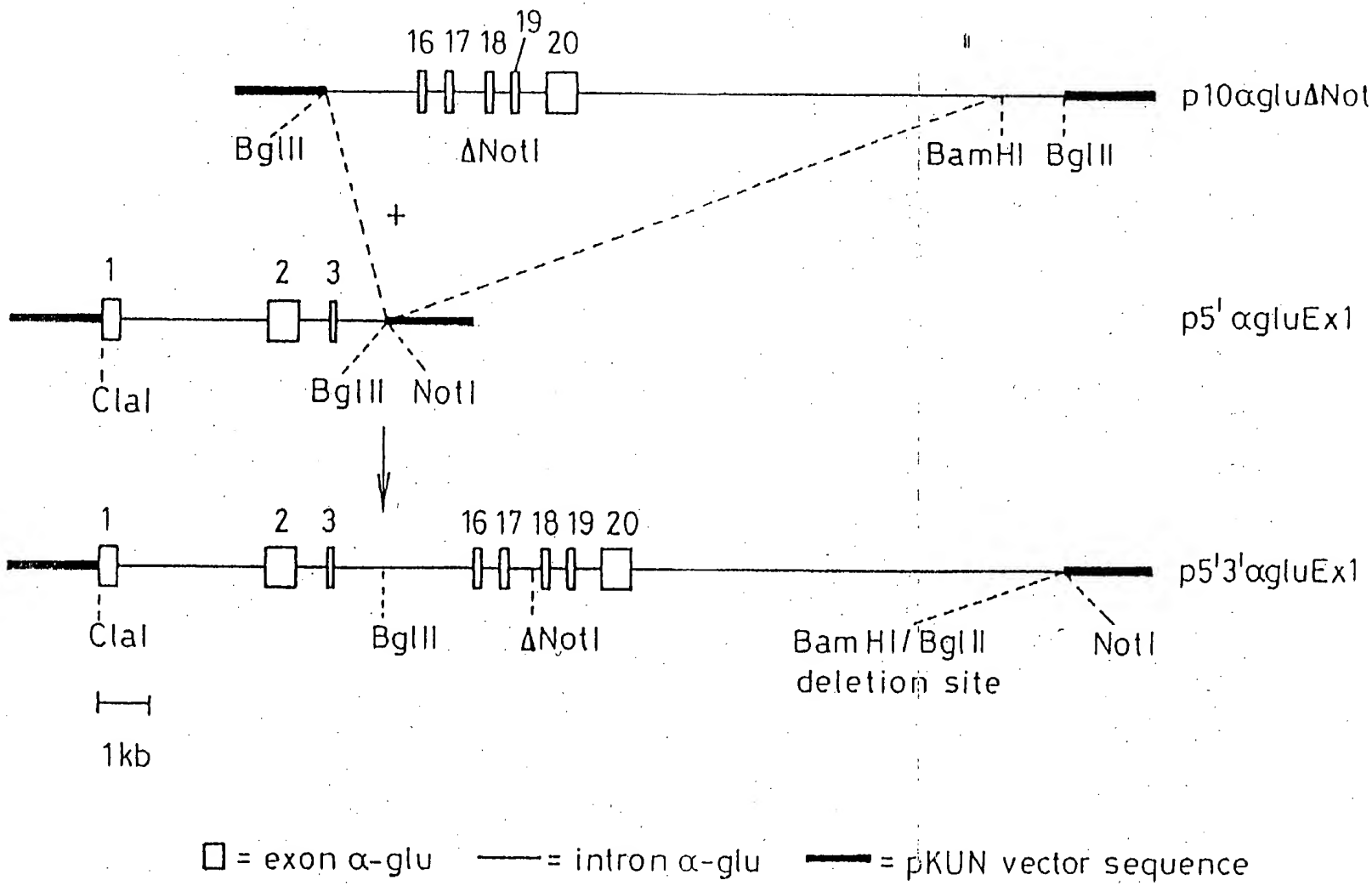


Fig. 3.C.

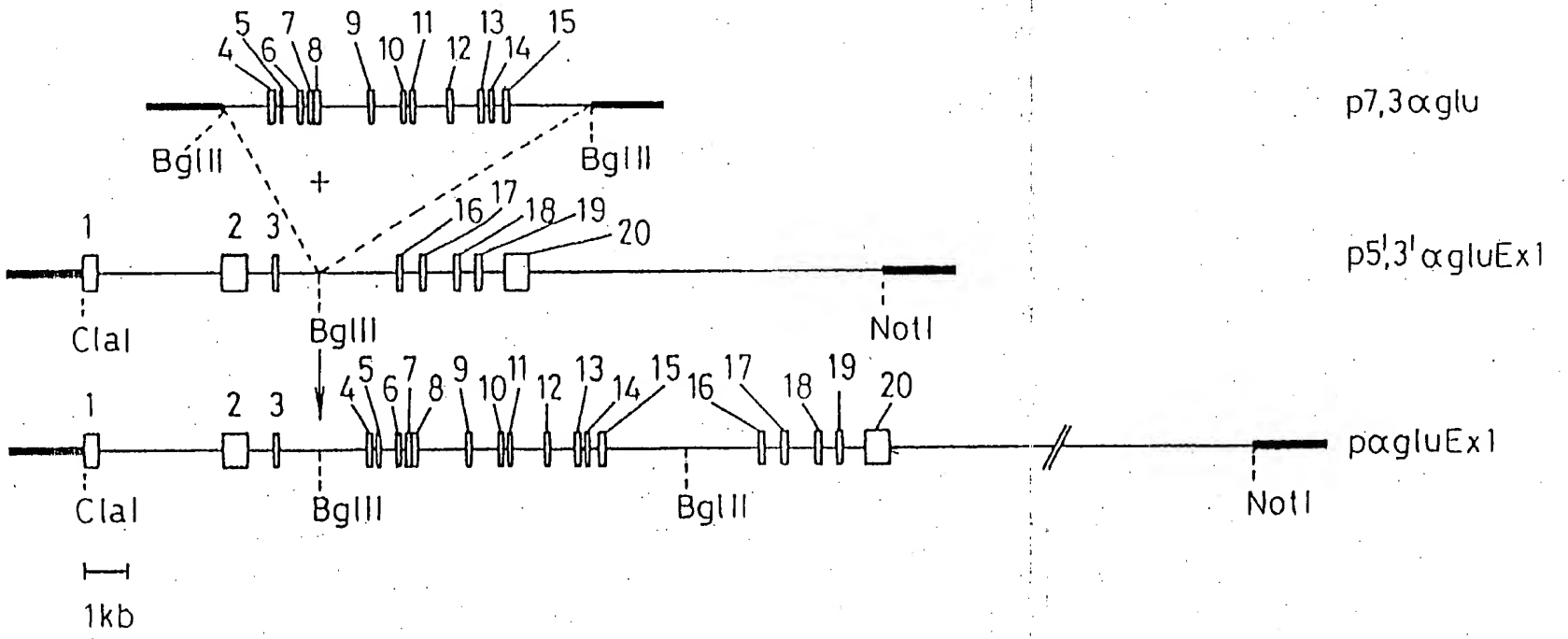

p7,3αglu
p5',3'αgluEx1
pαgluEx1
BglII
ClaI
NotI
1kb
□ = exon α-glu
—— = intron α-glu
━━ = pKUN vector sequence

Fig. 4. A.

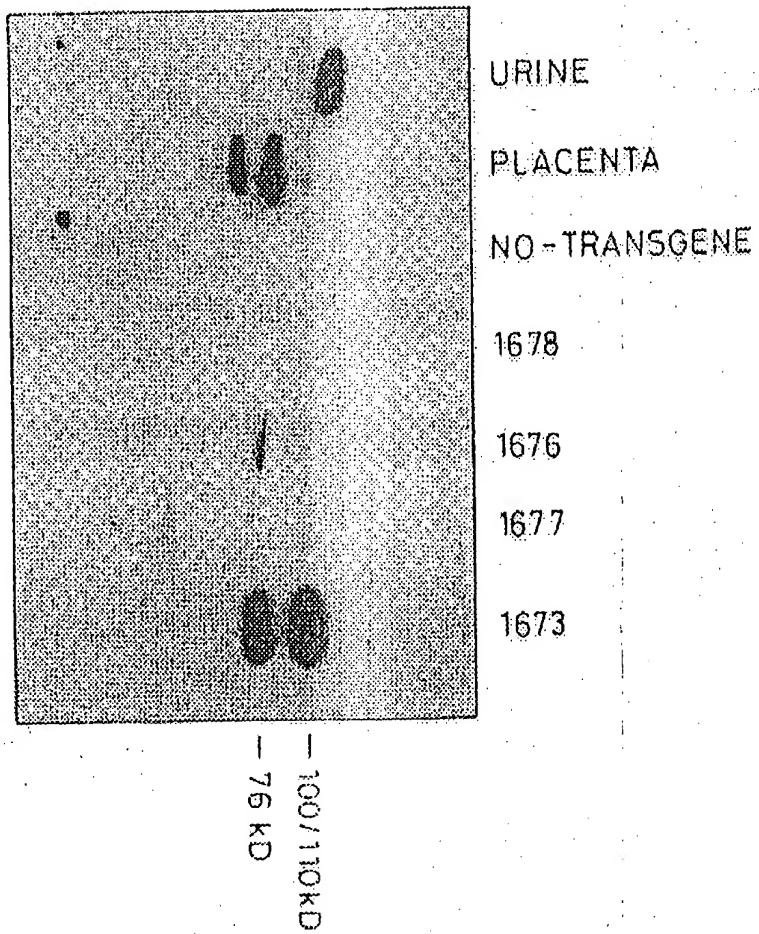
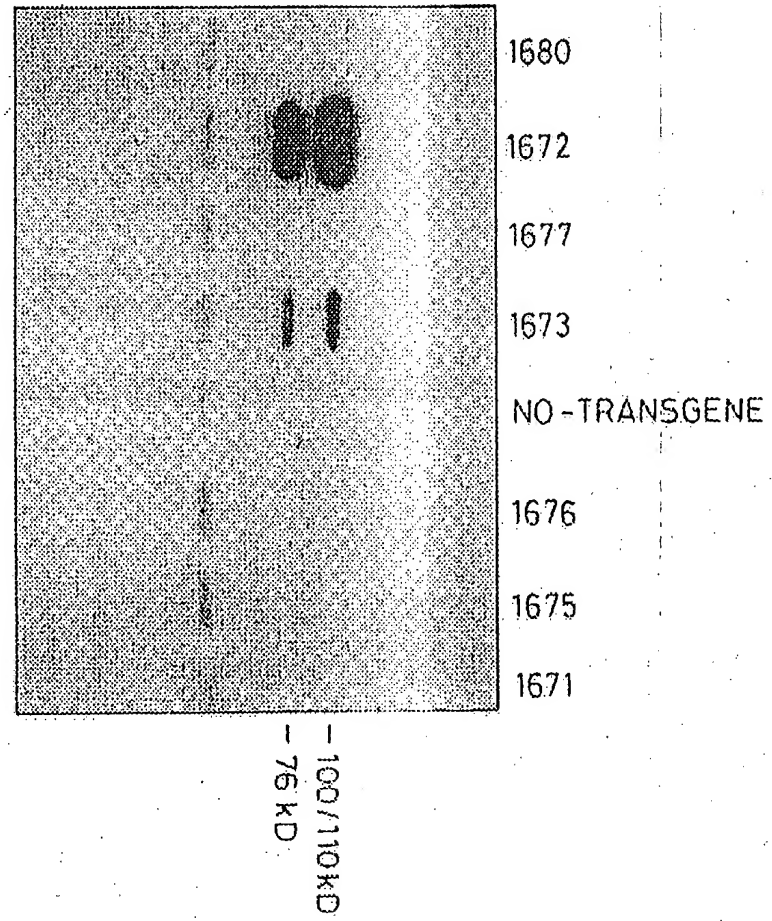


Fig. 4. B.



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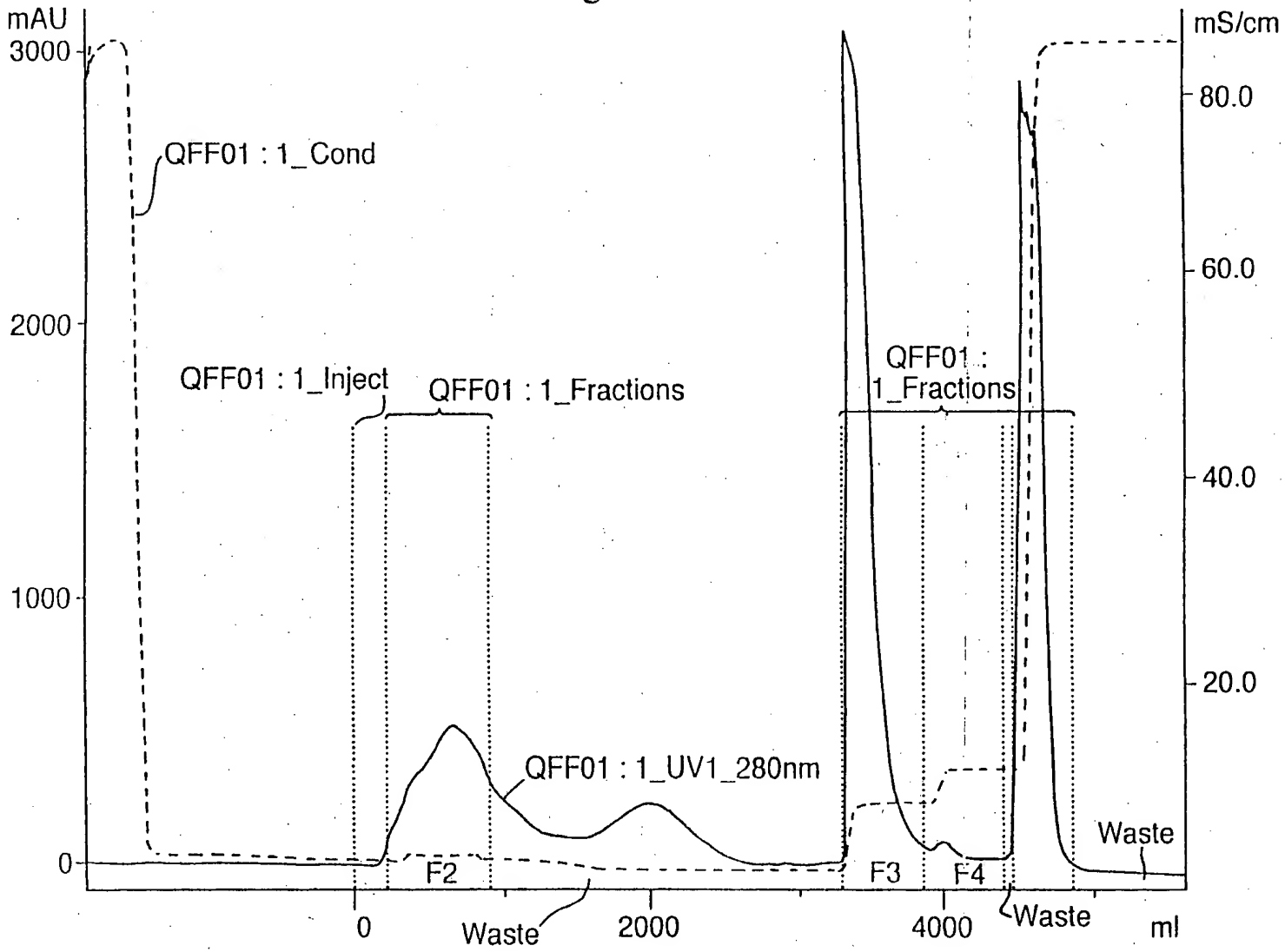


Fig. 6.

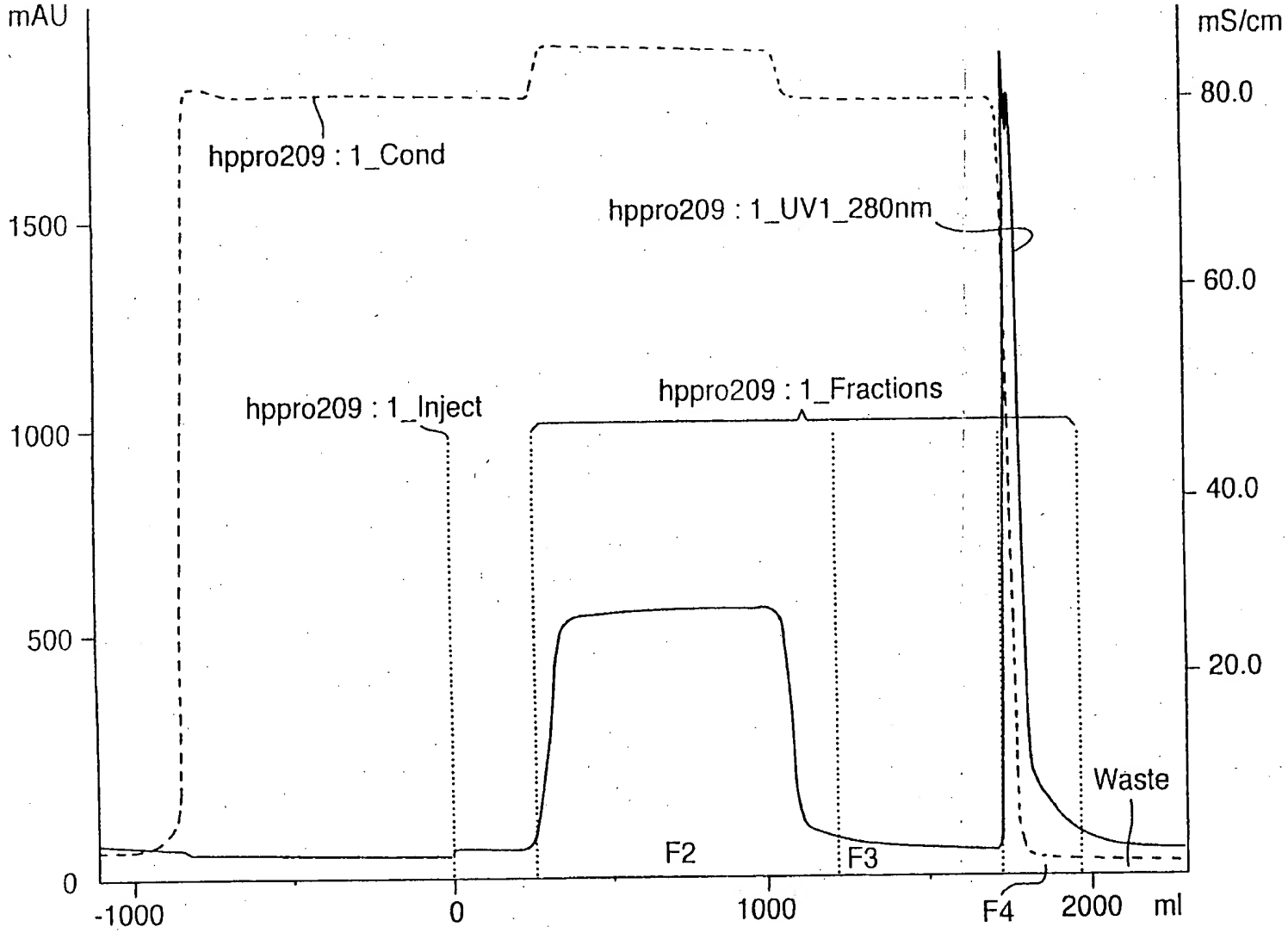
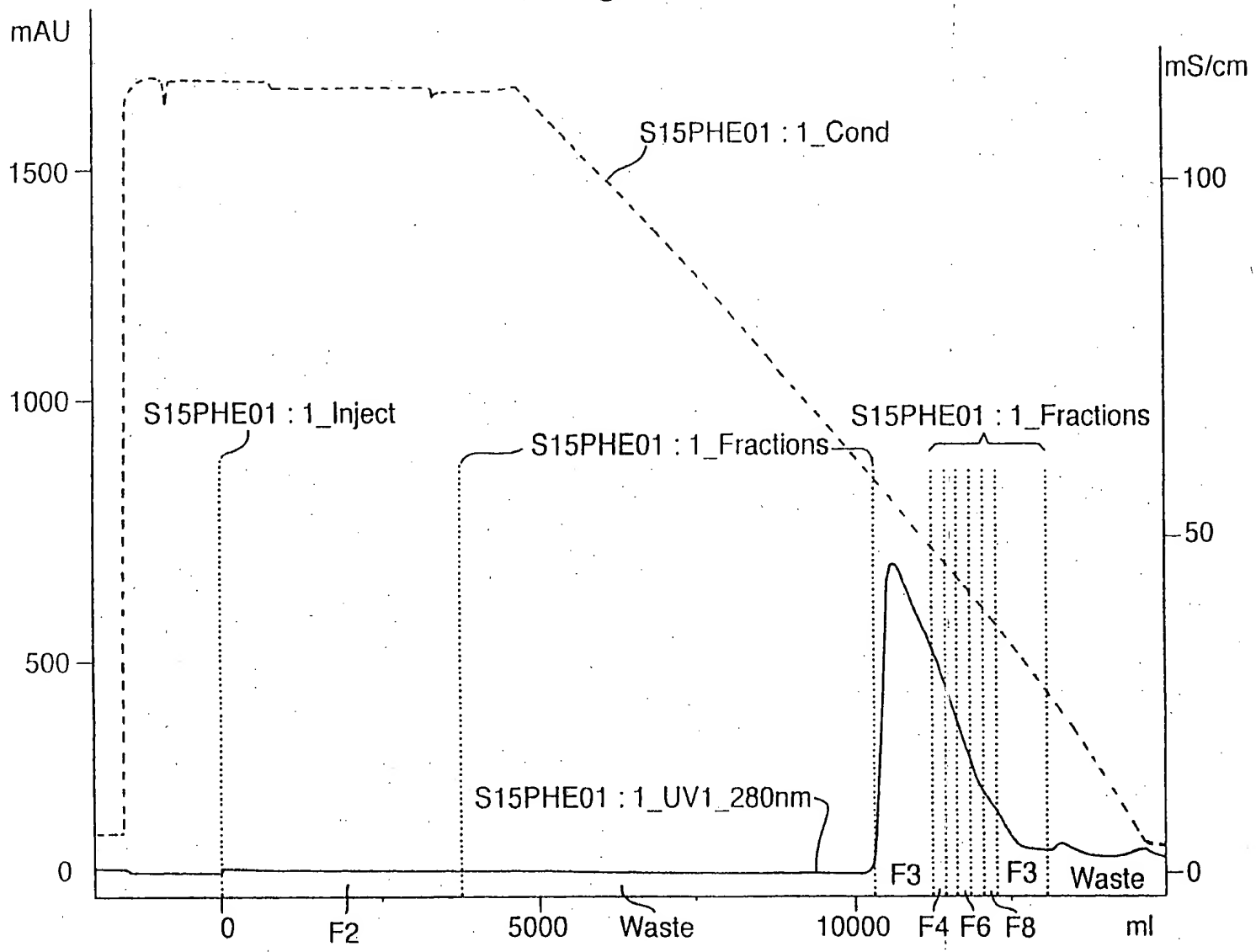


Fig. 7.



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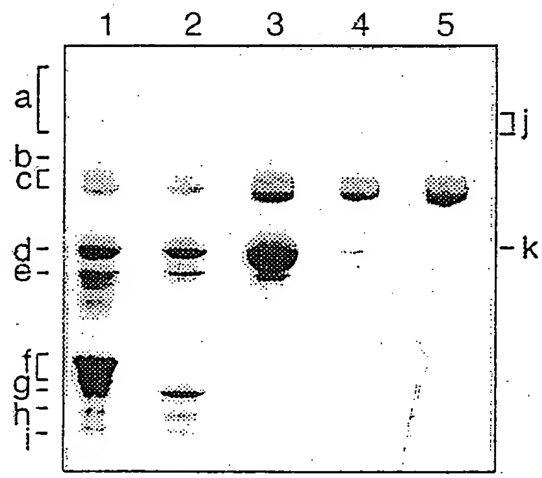

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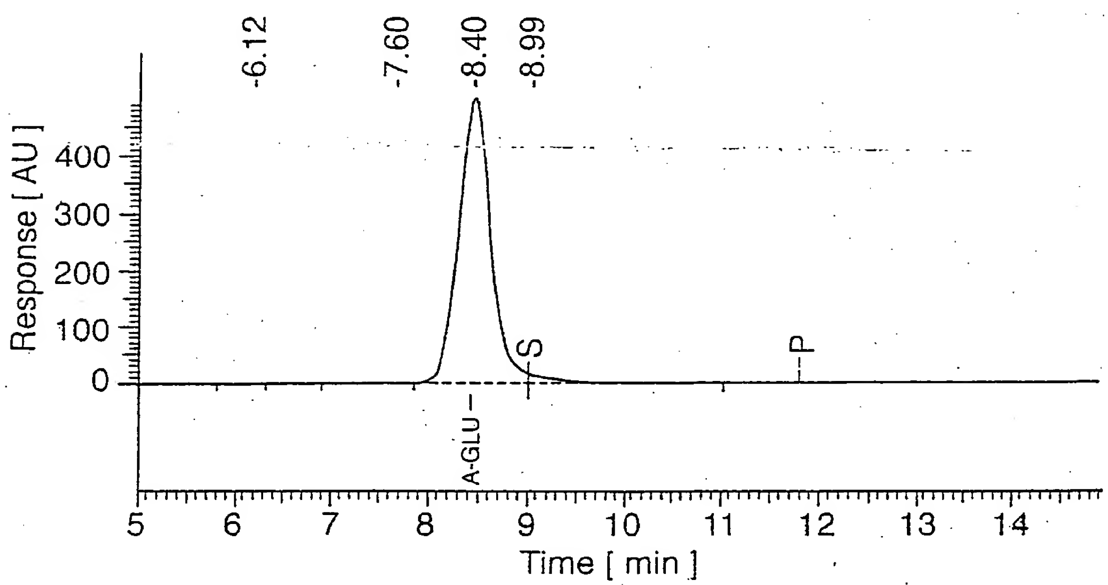

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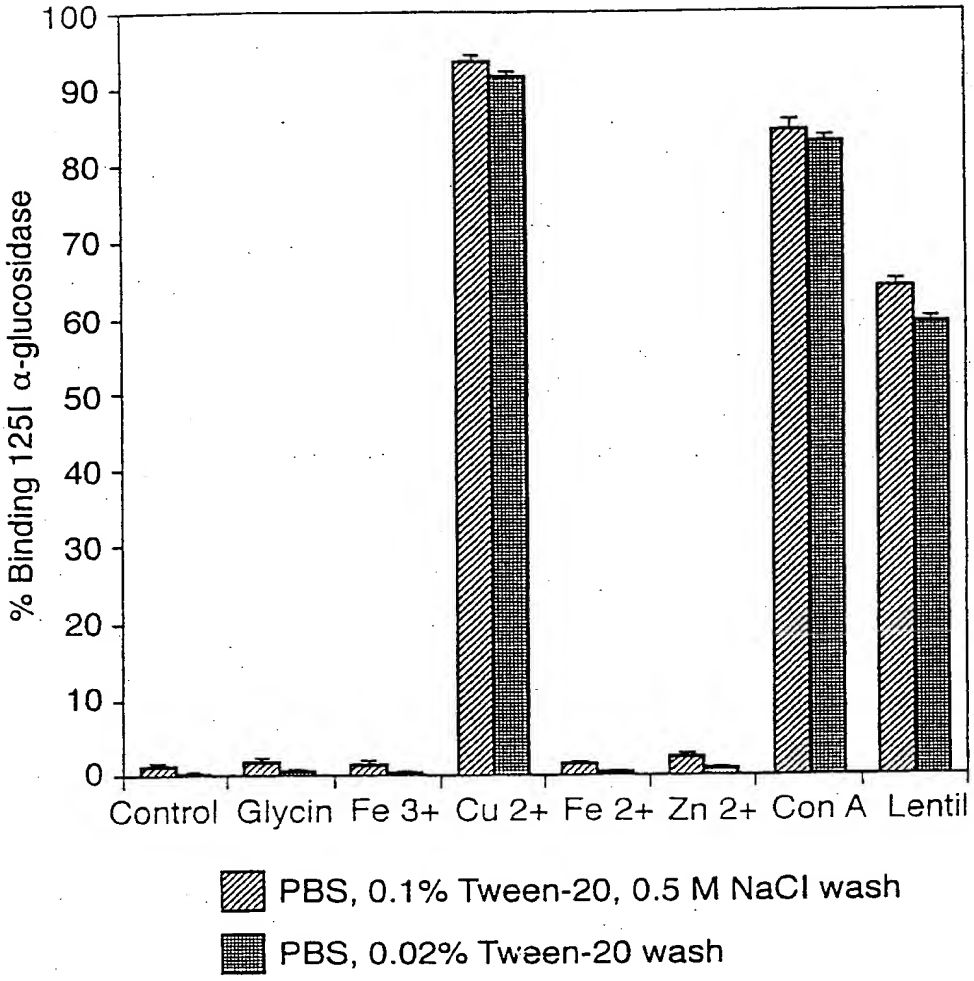


Fig. 11. A.

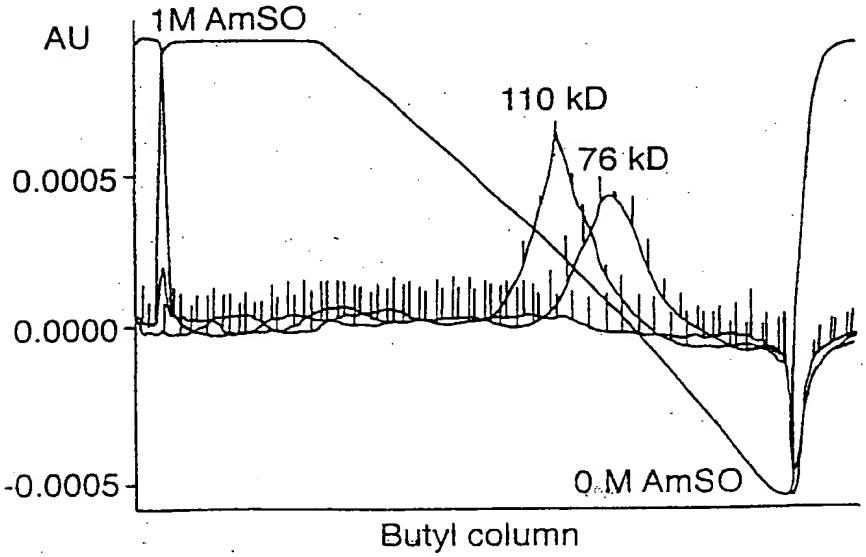


Fig. 11. B.

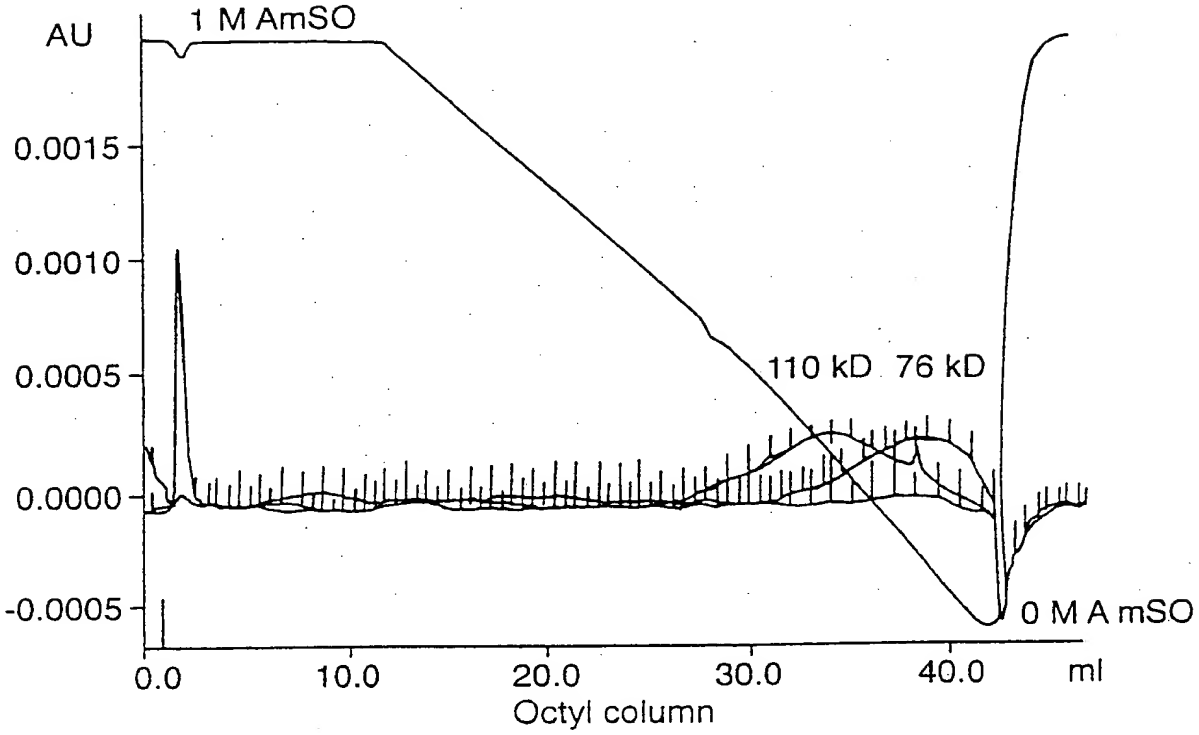


Fig. 11. C.

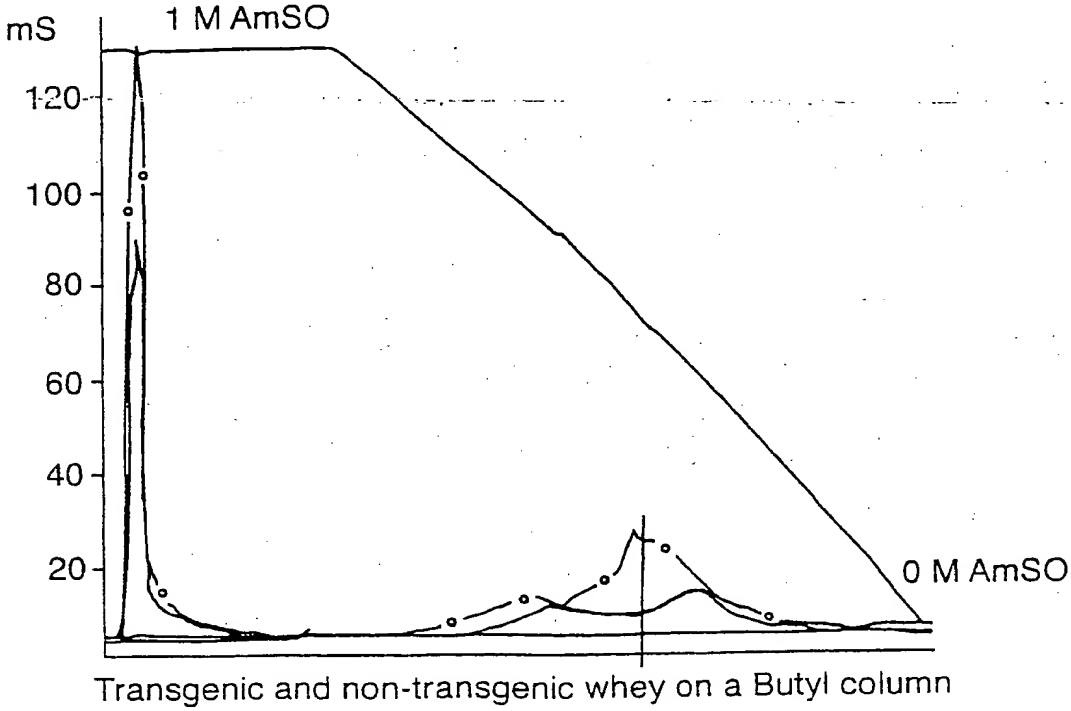


Fig. 11. D.

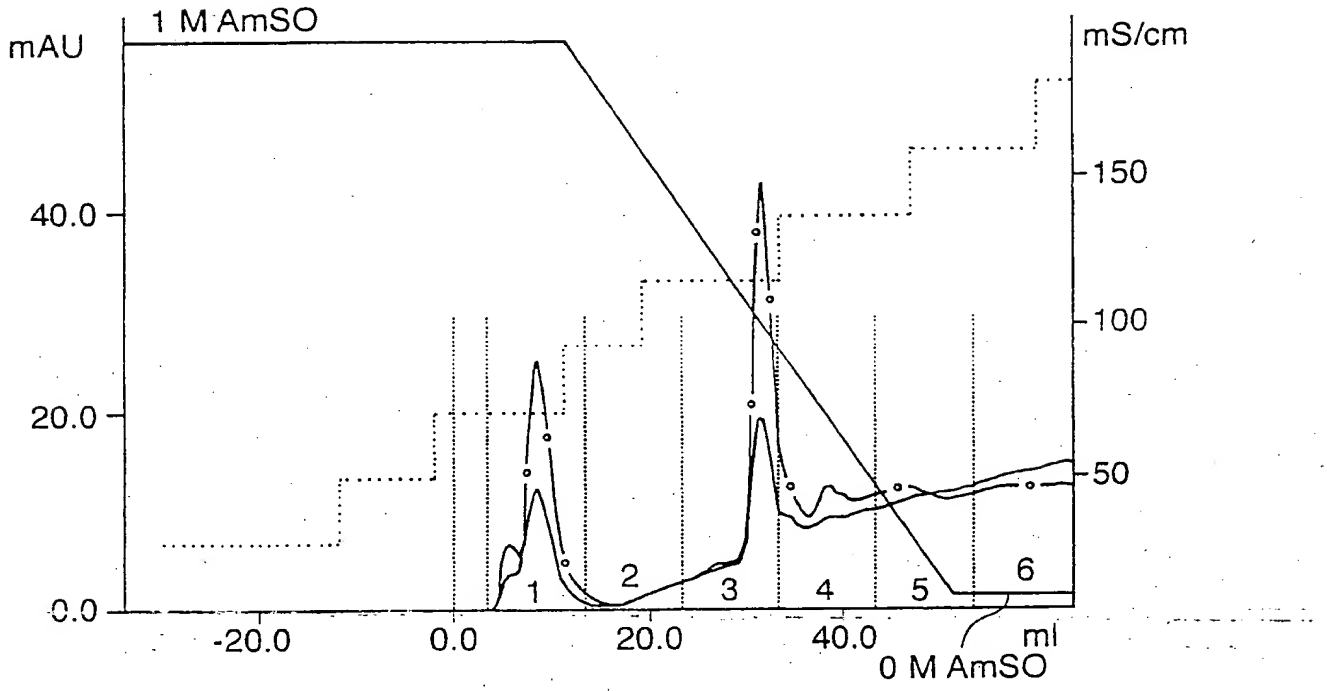

1 M AmSO
mAU
mS/cm
40.0
20.0
0.0
150
100
50
1
2
3
4
5
6
-20.0
0.0
20.0
40.0
ml
0 M AmSO

Fig. 12.

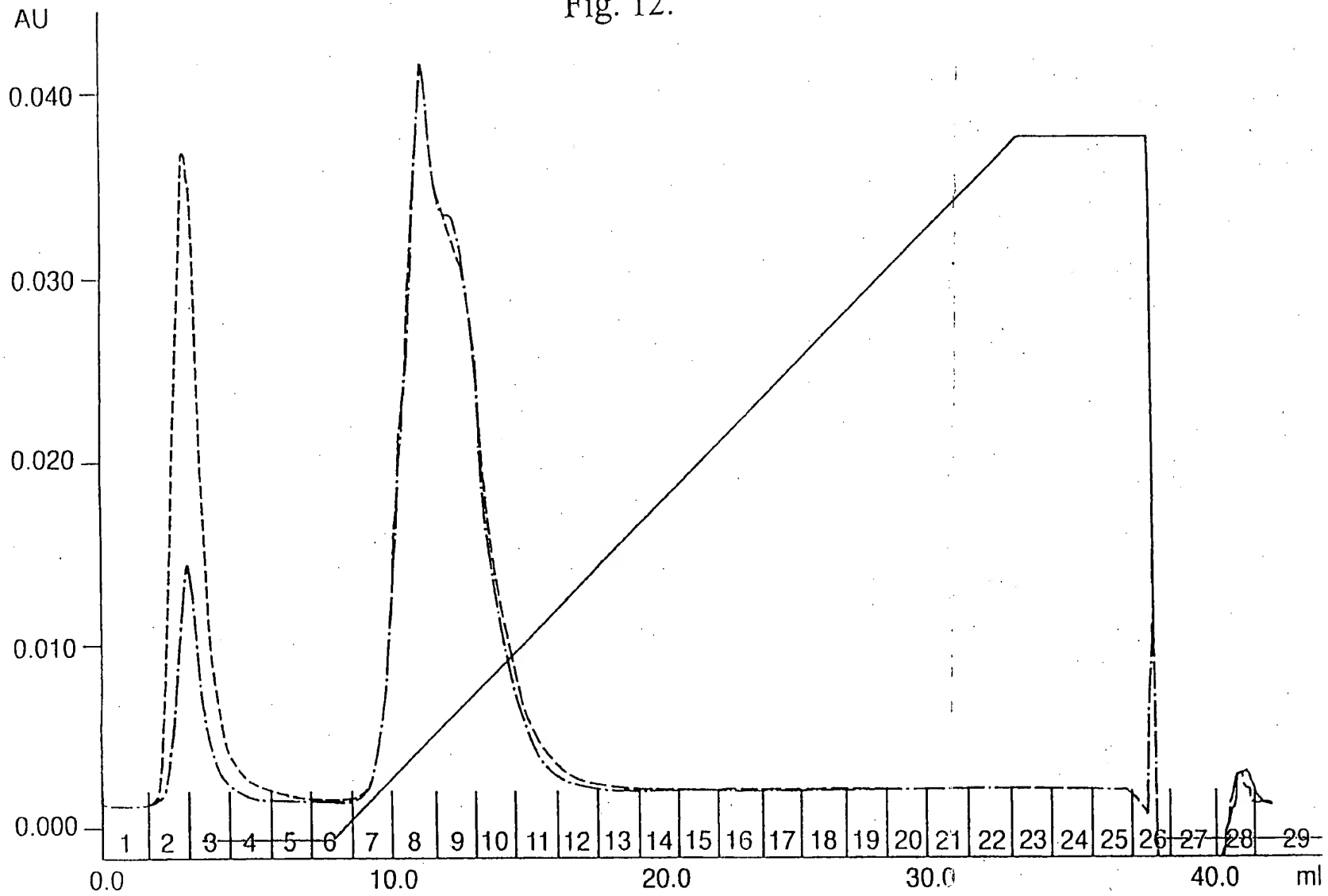


Fig. 13. A.

transgenic whey

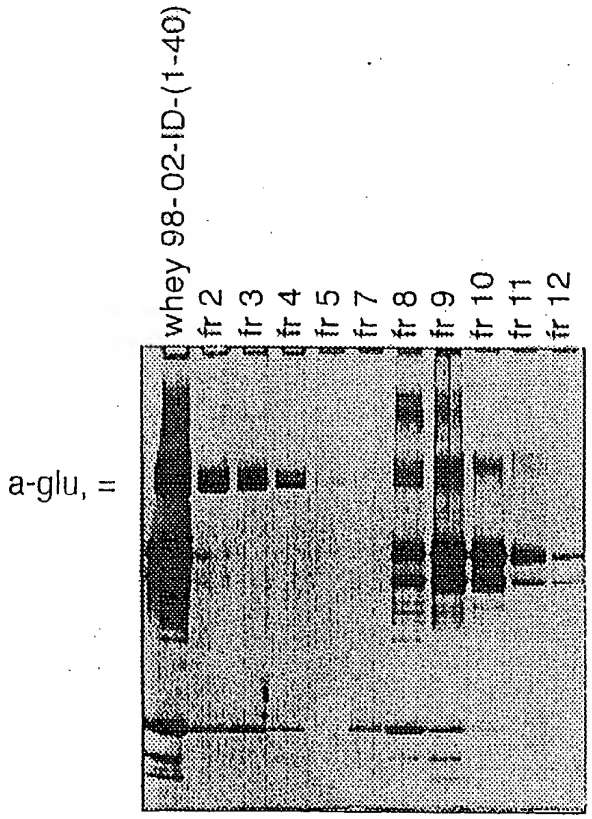


Fig. 13. B.

non-transgenic whey

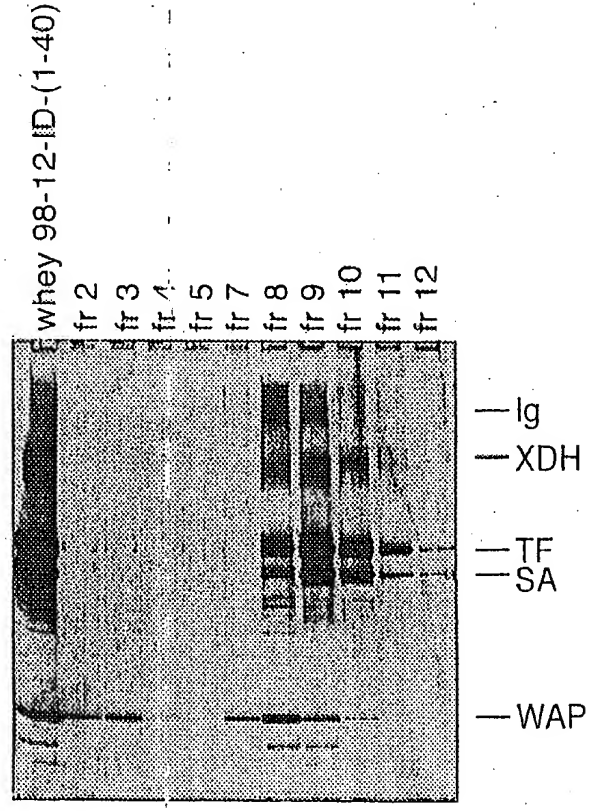


Fig. 14.

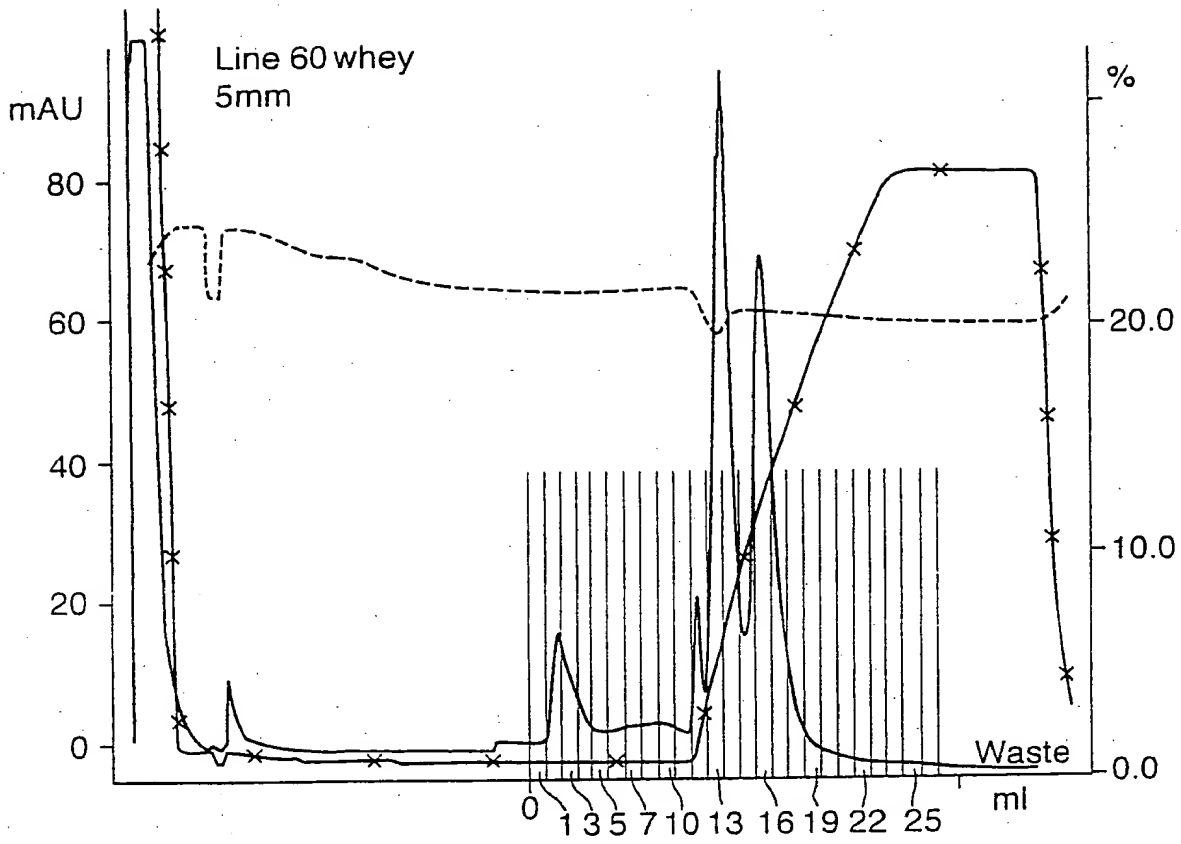
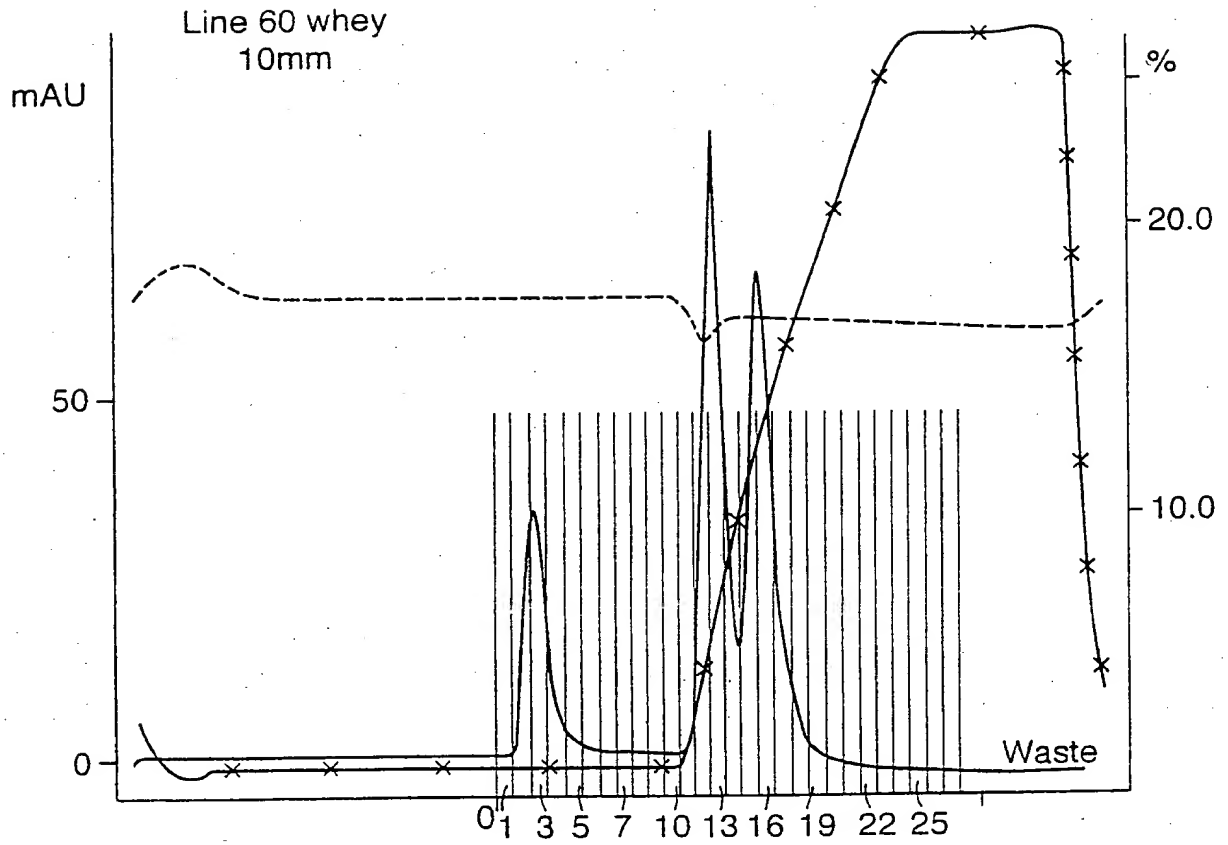

Line 60 whey
5mm
mAU
80
60
40
20
0
%
20.0
10.0
0.0
Waste
ml
0 1 3 5 7 10 13 16 19 22 25
12099801:1_UV1_280nm
12099801:1_pH
12099801:1_Cond%
12099801:1_Fractions

Fig. 15.



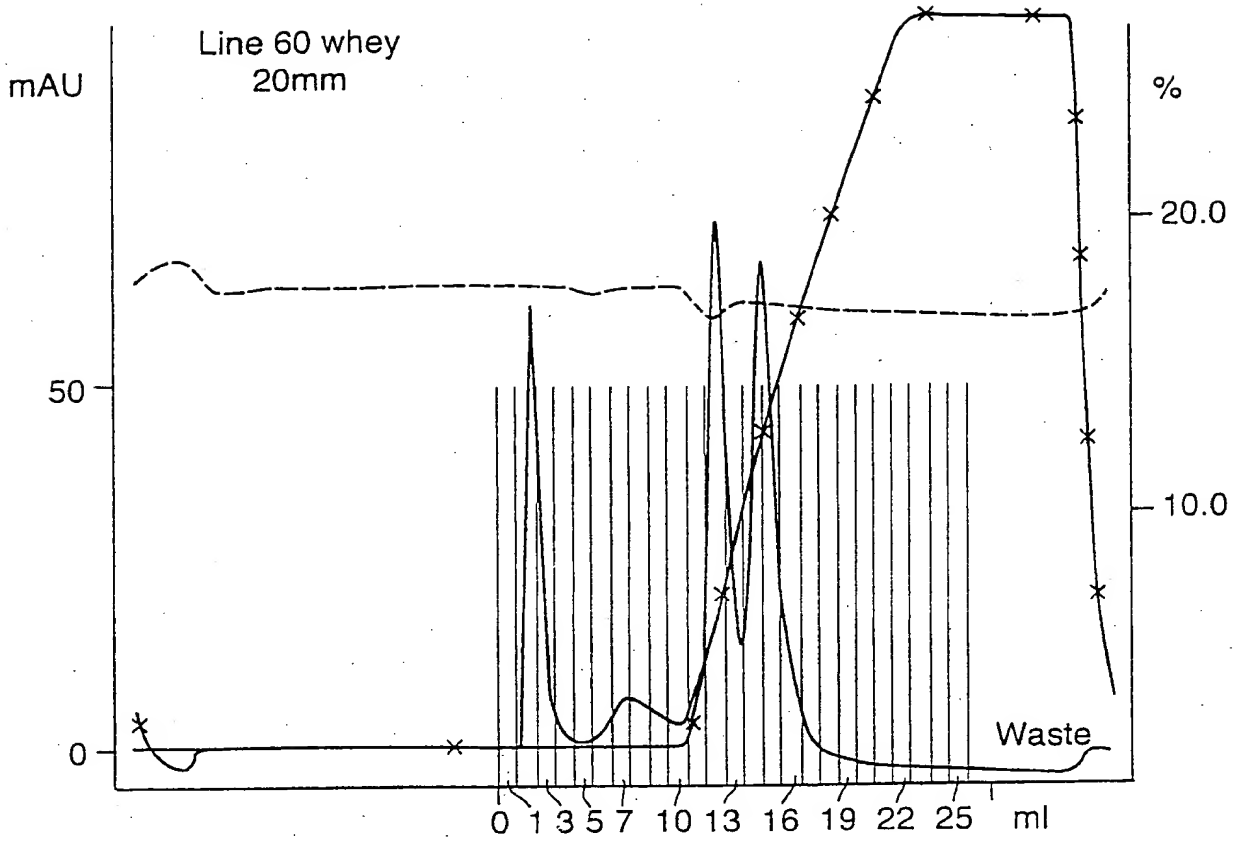
12099802:11_UV1_280nm

12099802:11_pH

12099802:11_Cond%

12099802:11_Fractions

Fig. 16.



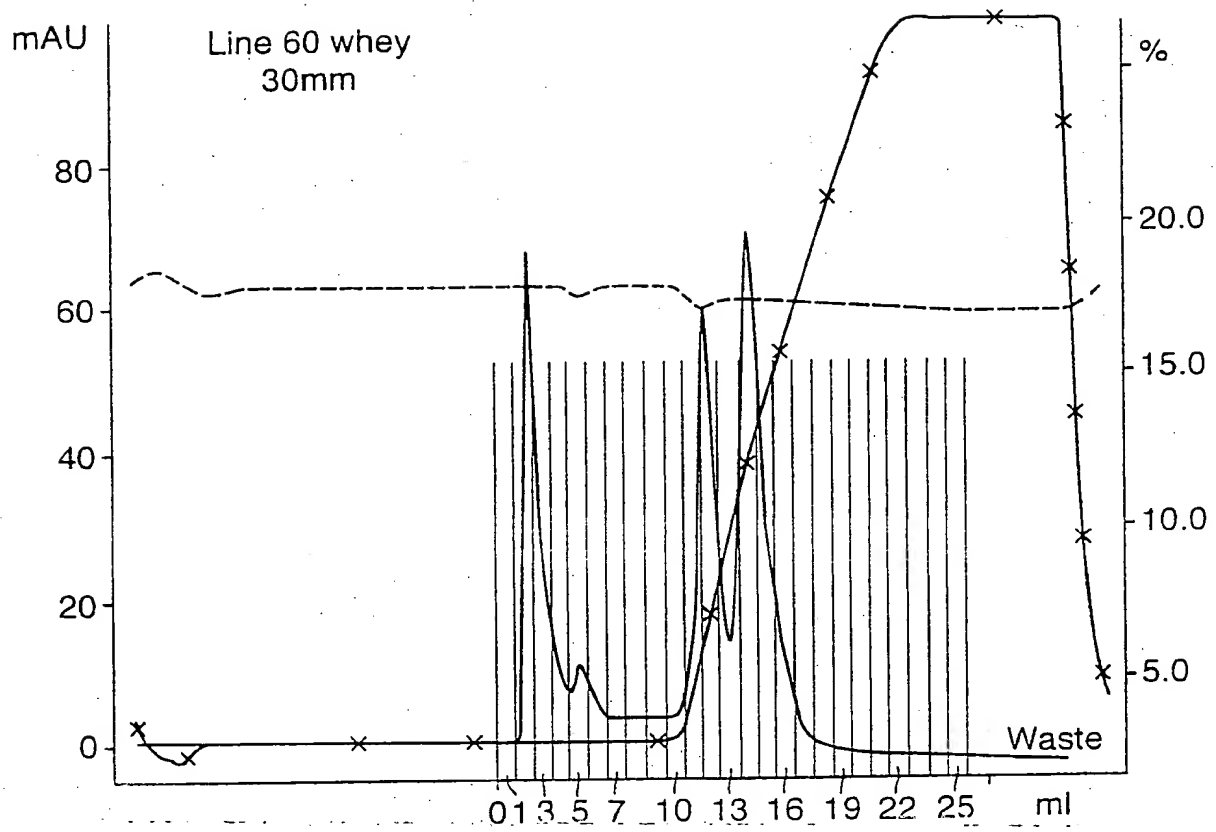
12099803:12_UV1_280nm

12099803:12_pH

12099803:12_Cond%

12099803:12_Fractions

Fig. 17.



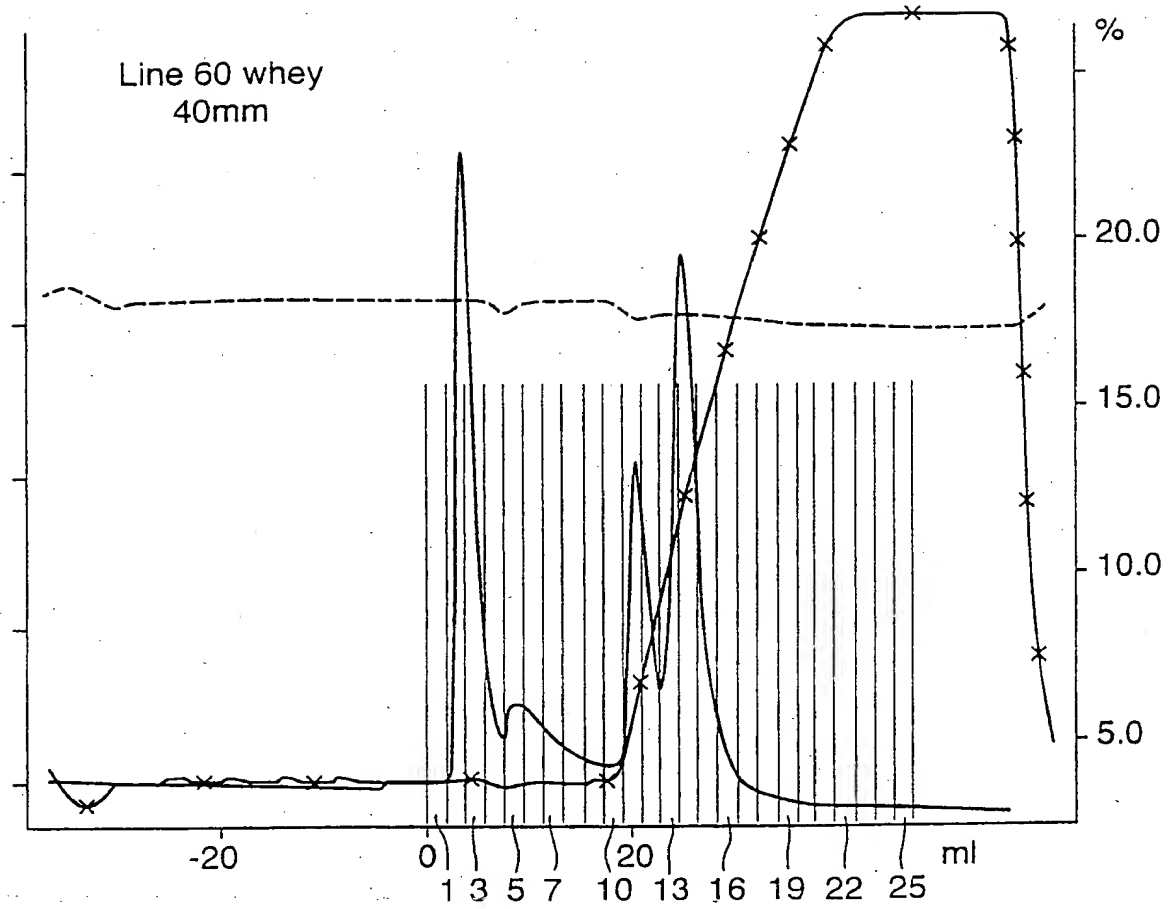
12099804:13_UV1_280nm

12099804:13_pH

12099804:13_Cond%

12099804:13_Fractions

Fig. 18.



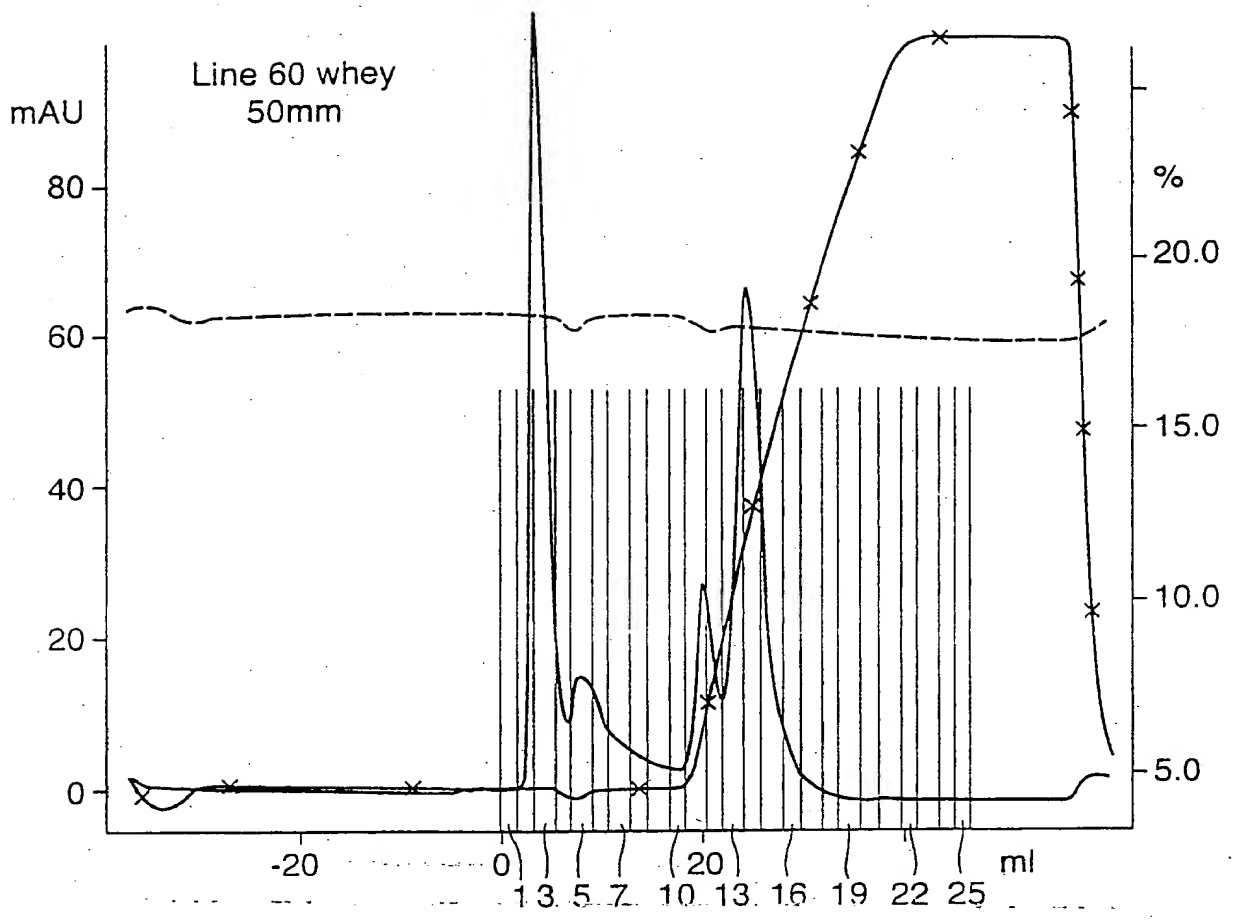
121099805:1_UV1_280nm

121099805:1_pH

121099805:1_Cond%

121099805:1_Fractions

Fig. 19.



121099806:1_UV1_280nm

121099806:1_pH

121099806:1_Cond%

121099806:1_Fractions

Fig. 20.

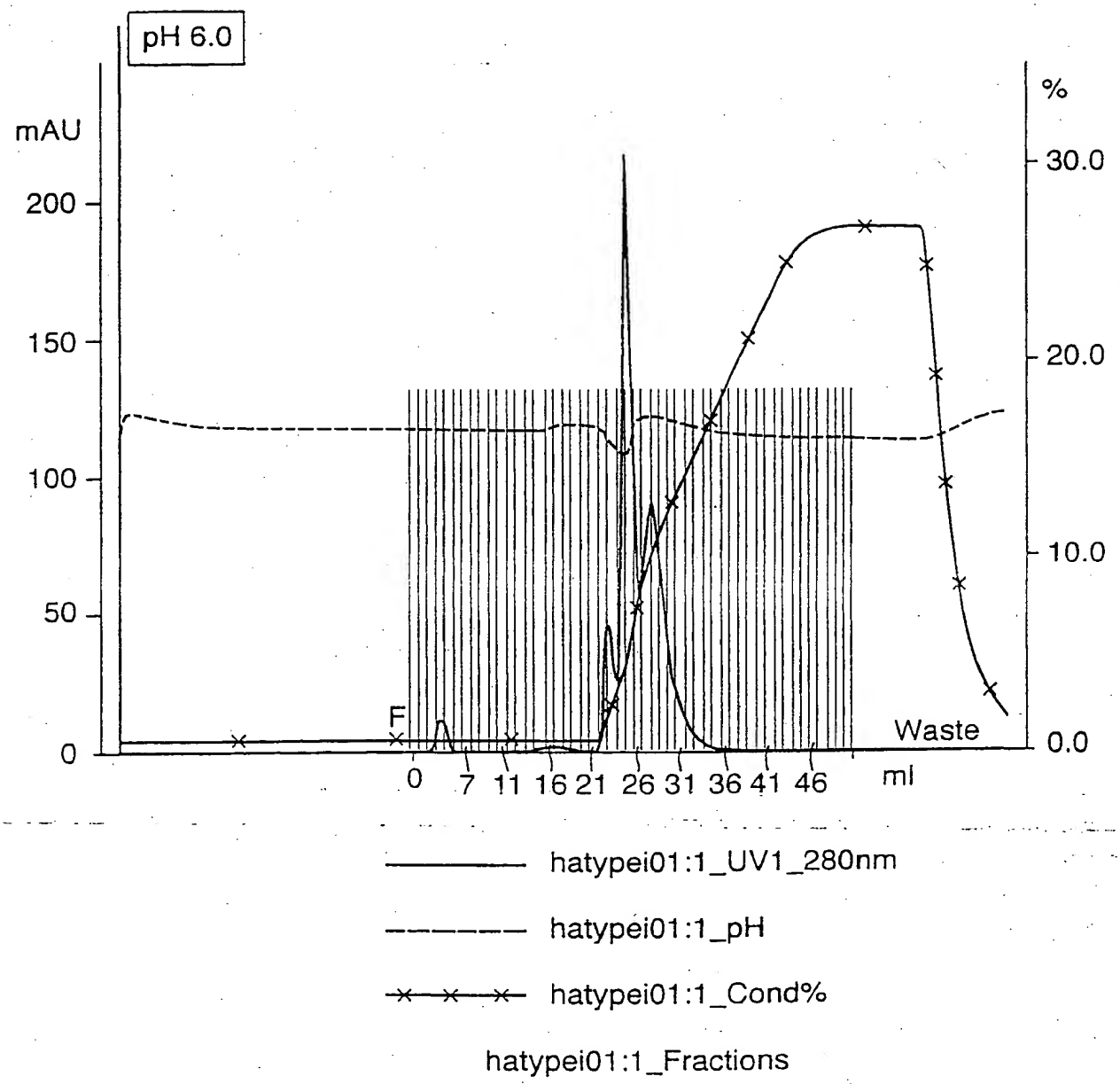

pH 6.0
mAU
200
150
100
50
0
%
30.0
20.0
10.0
0.0
F
Waste
0
7
11
16
21
26
31
36
41
46
ml
hatypei01:1_UV1_280nm
hatypei01:1_pH
hatypei01:1_Cond%
hatypei01:1_Fractions

Fig. 21.

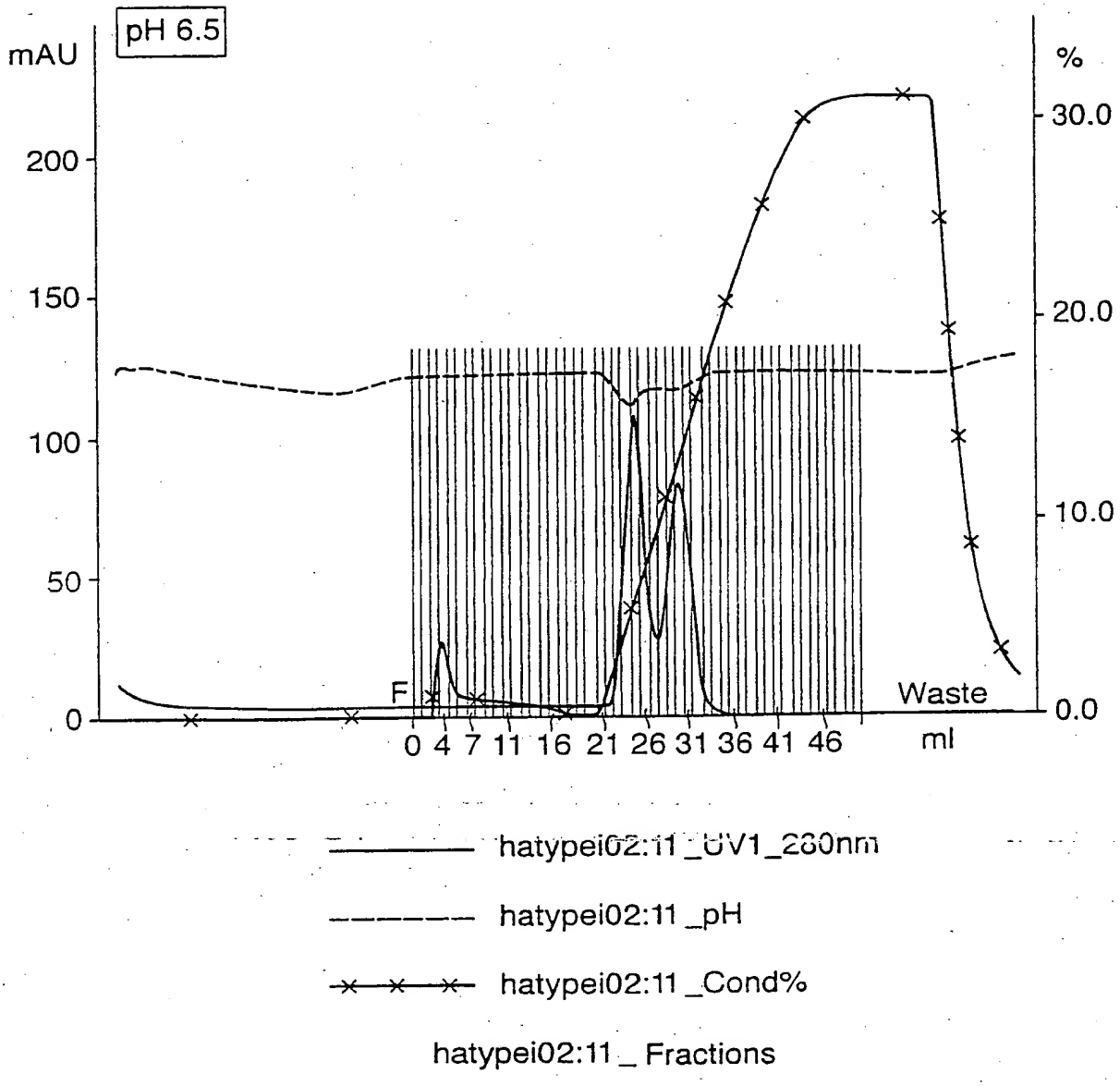
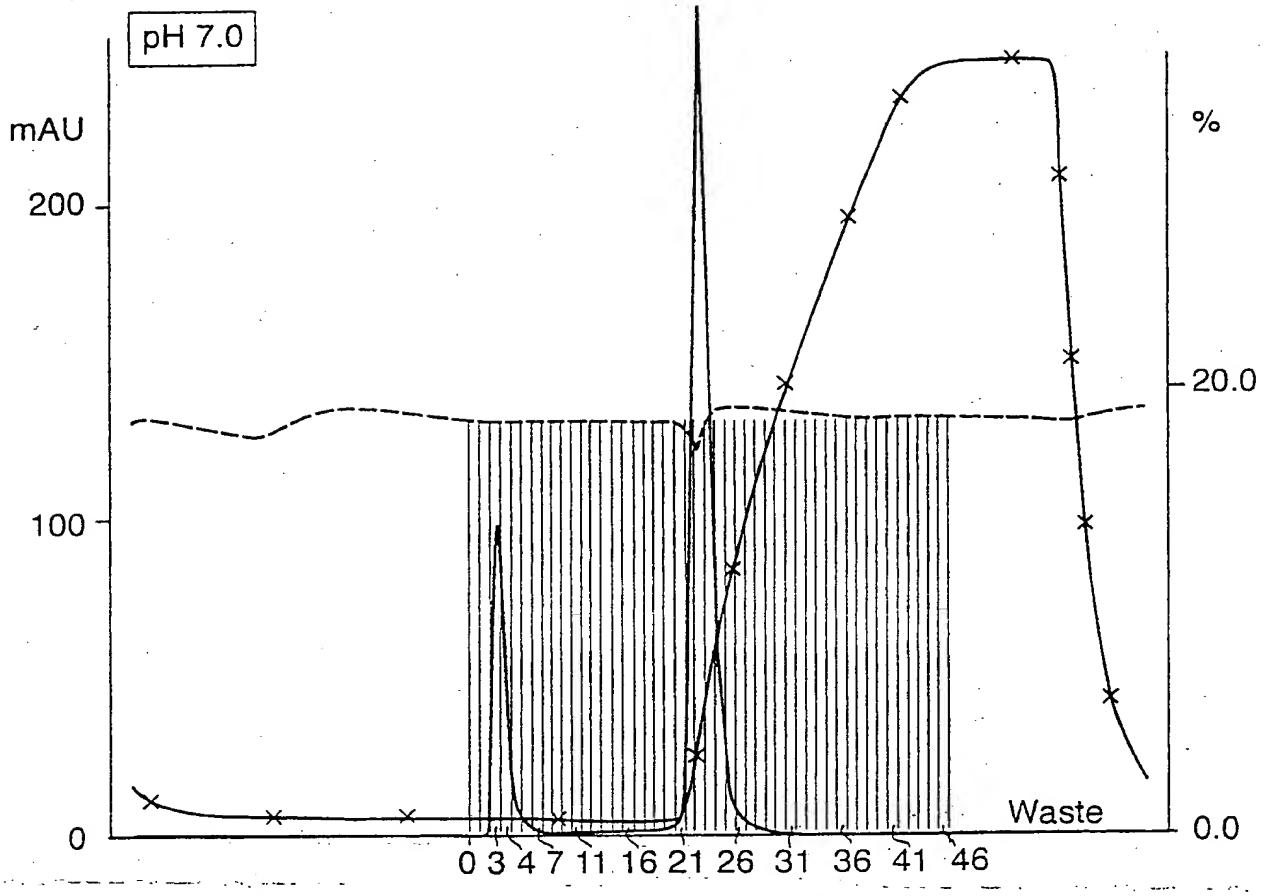

pH 6.5
mAU
200
150
100
50
0
%
30.0
20.0
10.0
0.0
F
Waste
0 4 7 11 16 21 26 31 36 41 46
ml
hatypei02:11 _UV1_280nm
hatypei02:11 _pH
hatypei02:11 _Cond%
hatypei02:11 _ Fractions

Fig. 22.



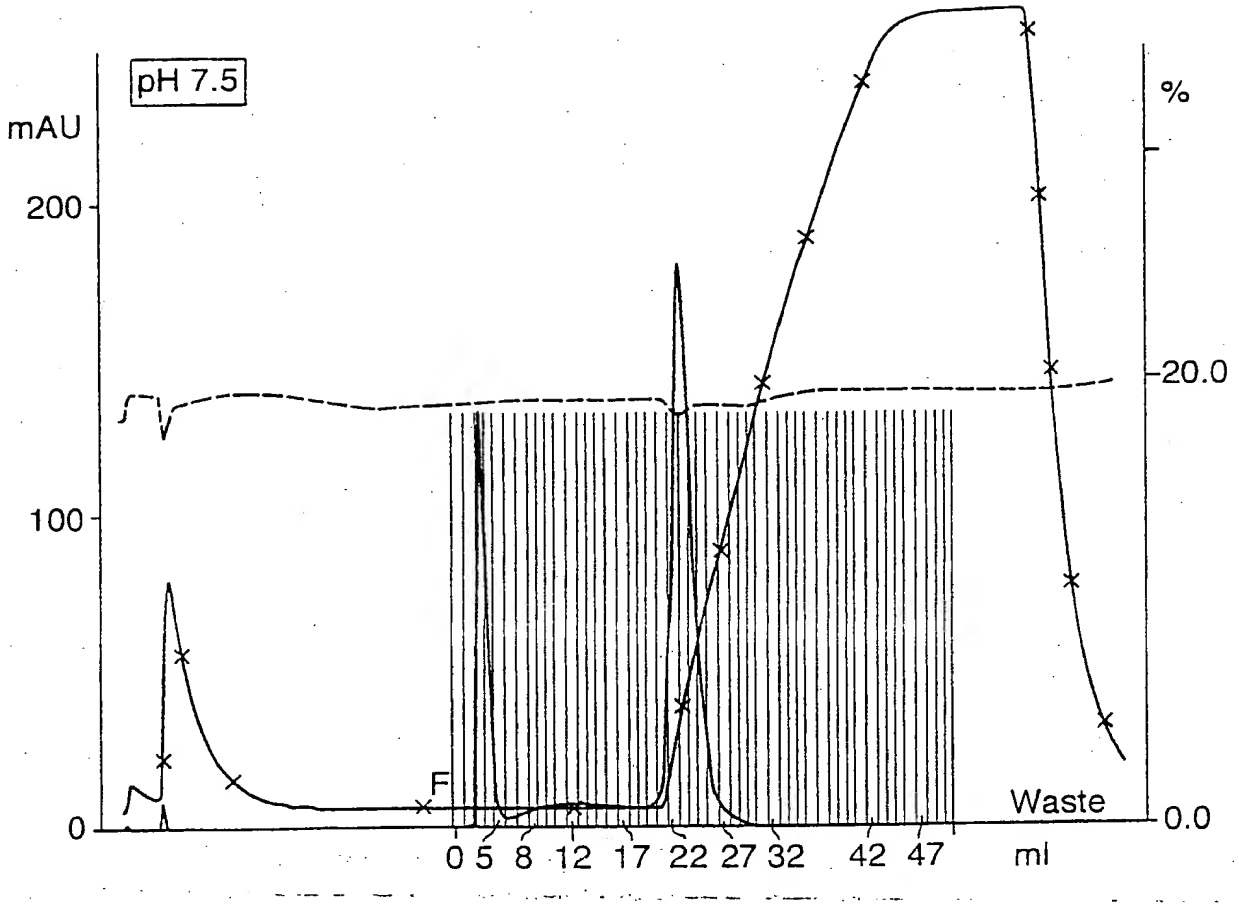
hatypei03:12_UV1_280nm

hatypei03:12_pH

hatypei03:12_Cond%

hatypei03:12_ Fractions

Fig. 23.



hatypei04:13 _UV1_280nm

hatypei04:13 _pH

hatypei04:13 _Cond%

hatypei04:13 _ Fractions

Fig. 24.

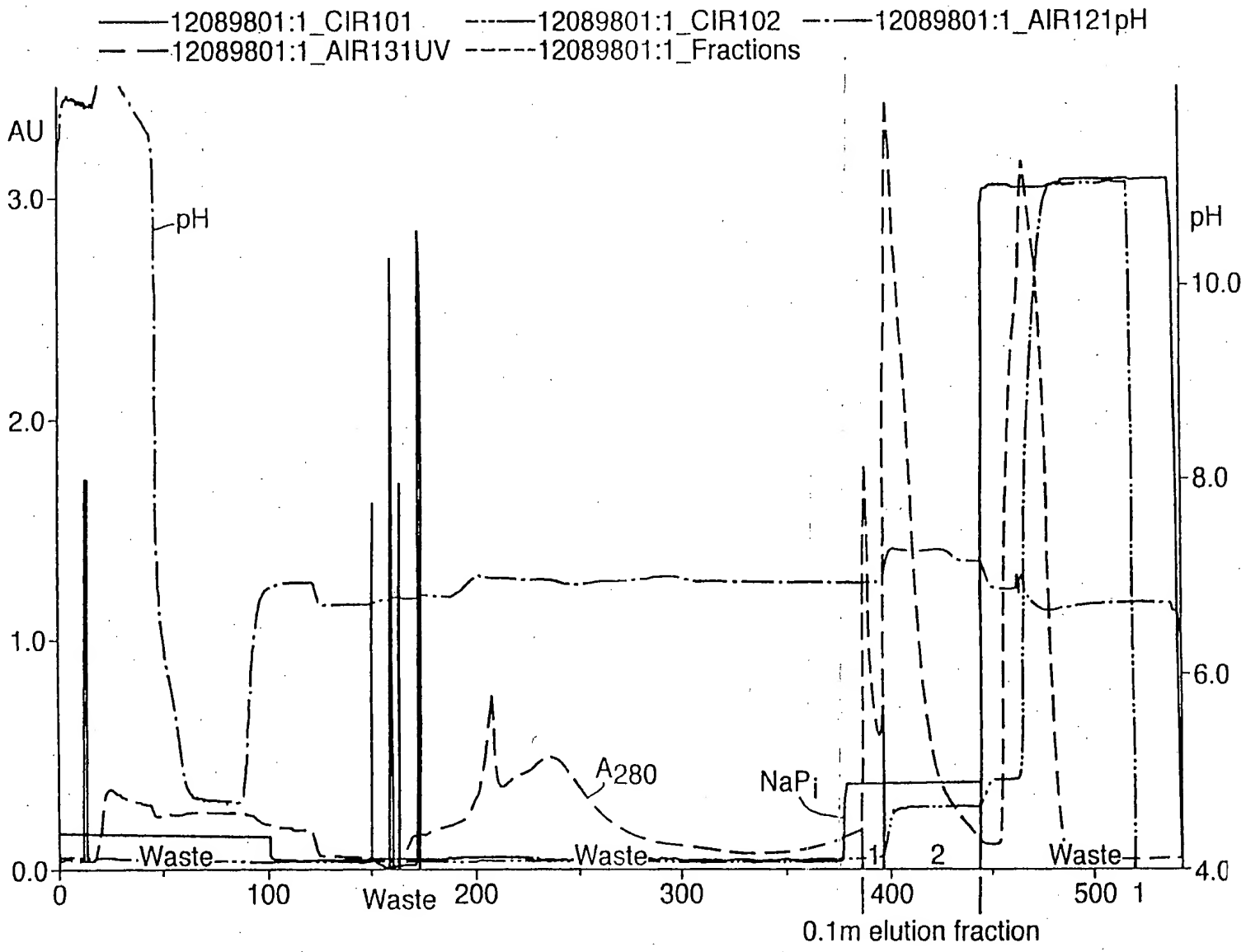


Fig. 25.

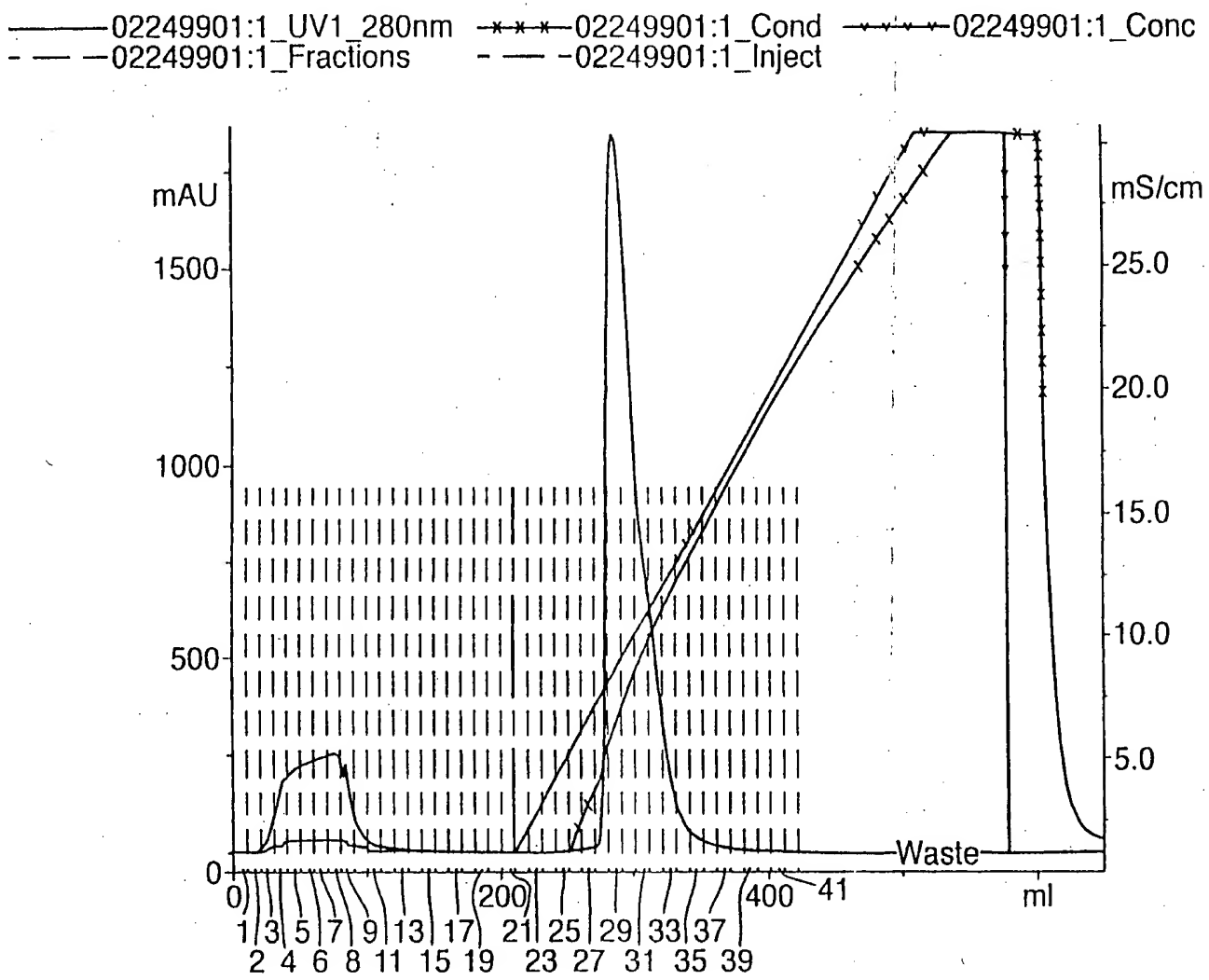
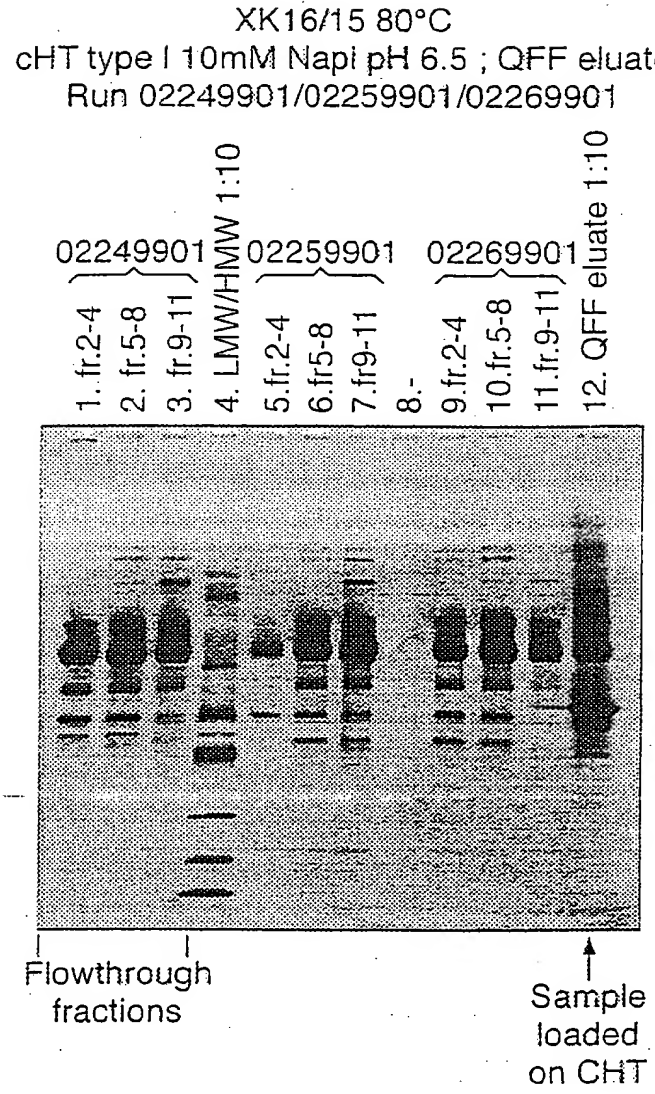


Fig. 26.


XK16/15 80°C
cHT type I 10mM NaPi pH 6.5 ; QFF eluate
Run 02249901/02259901/02269901
02249901
02259901
02269901
1. fr.2-4
2. fr.5-8
3. fr.9-11
4. LMW/HMW 1:10
5.fr.2-4
6.fr5-8
7.fr9-11
8.-
9.fr.2-4
10.fr.5-8
11.fr.9-11
12. QFF eluate 1:10
Flowthrough fractions
Sample loaded on CHT